

Resource Summary Report

Generated by [kravitz2](#) on Jul 31, 2026

PhyloBayes

RRID:SCR_006402

Type: Tool

Proper Citation

PhyloBayes (RRID:SCR_006402)

Resource Information

URL: <http://megasun.bch.umontreal.ca/People/lartillot/www/>

Proper Citation: PhyloBayes (RRID:SCR_006402)

Description: A Bayesian Monte Carlo Markov Chain (MCMC) sampler software for phylogenetic reconstruction. Its main distinguishing feature is the underlying probabilistic model, CAT (Lartillot and Philippe, 2004). CAT is an infinite mixture model accounting for site-specific amino-acid or nucleotide preferences. It is well suited to phylogenomic studies using large multigene alignments., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: PhyloBayes

Synonyms: PhyloBayes - phylogenetic reconstruction using infinite mixtures

Resource Type: software resource

Defining Citation: [PMID:24318999](#)

Keywords: phylogenomic, multigene alignment, alignment, reconstruction

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: PhyloBayes

Resource ID: SCR_006402

Alternate IDs: OMICS_02212

Record Creation Time: 20220129T080236+0000

Record Last Update: 20260725T190622+0000

Ratings and Alerts

No rating or validation information has been found for PhyloBayes.

No alerts have been found for PhyloBayes.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 485 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#).

Pietluch F, et al. (2025) Dating the Origin and Spread of Plastids and Chromatophores. *International journal of molecular sciences*, 26(12).

Lavrov DV, et al. (2025) Pervasive Mitochondrial tRNA Gene Loss in Clade B of Haplosclerid Sponges (Porifera, Demospongiae). *Genome biology and evolution*, 17(3).

Jeong JS, et al. (2025) Complete mitochondrial genome of the world's most endangered tern, *Thalasseus bernsteini*, and a mitogenomic phylogenetic study of the Laridae family. *Scientific reports*, 15(1), 29326.

Liu Q, et al. (2025) Comparative Mitogenomes and Phylogenetic Analyses of Coccinellidae (Coleoptera: Coccinelloidea). *Ecology and evolution*, 15(3), e71053.

Martin ?íhová J, et al. (2025) An obligate symbiont of *Haematomyzus elephantis* with a strongly reduced genome resembles symbiotic bacteria in sucking lice. *Applied and environmental microbiology*, 91(6), e0022025.

Zhao T, et al. (2025) Evolutionary history and divergence times of Tettigoniidae (Orthoptera) inferred from mitochondrial phylogenomics. *Frontiers in genetics*, 16, 1495754.

Abalde S, et al. (2025) A Phylogenomic Backbone for Acoelomorpha Inferred From Transcriptomic Data. *Systematic biology*, 74(1), 70.

Giacomelli M, et al. (2025) CAT-Posterior Mean Site Frequencies Improves Phylogenetic Modeling Under Maximum Likelihood and Resolves Tardigrada as the Sister of Arthropoda Plus Onychophora. *Genome biology and evolution*, 17(1).

Zhu P, et al. (2025) Comparative and Phylogenetic Analyses of Mitochondrial Genomes in Carabidae (Coleoptera: Adephaga). *Ecology and evolution*, 15(7), e71707.

Yabuki A, et al. (2025) Massive RNA Editing in Ascetosporean Mitochondria. *Microbes and environments*, 40(1).

Santana-Molina C, et al. (2025) Chimeric origins and dynamic evolution of central carbon metabolism in eukaryotes. *Nature ecology & evolution*, 9(4), 613.

Shazib SUA, et al. (2025) Phylogeny and species delimitation of ciliates in the genus *Spirostomum* (class Heterotrichea) using single-cell transcriptomes. *BMC ecology and evolution*, 25(1), 17.

Goremykin V, et al. (2025) ?High-level phylogenetic relationships within Pezizomycotina revisited. *IMA fungus*, 16, e153279.

Dai J, et al. (2024) The First Two Complete Mitochondrial Genomes for the Subfamily Meligethinae (Coleoptera: Nitidulidae) and Implications for the Higher Phylogeny of Nitidulidae. *Insects*, 15(1).

Boden JS, et al. (2024) Timing the evolution of phosphorus-cycling enzymes through geological time using phylogenomics. *Nature communications*, 15(1), 3703.

Petitgas C, et al. (2024) Metabolic and neurobehavioral disturbances induced by purine recycling deficiency in *Drosophila*. *eLife*, 12.

Klirs Y, et al. (2024) Evolutionary Insights from the Mitochondrial Genome of *Oikopleura dioica*: Sequencing Challenges, RNA Editing, Gene Transfers to the Nucleus, and tRNA Loss. *Genome biology and evolution*, 16(9).

Kaur T, et al. (2024) Discovery of a novel *Wolbachia* in *Heterodera* expands nematode host distribution. *Frontiers in microbiology*, 15, 1446506.

Galindo LJ, et al. (2024) Transcriptomics of Diphyllatea (CRuMs) from South Pacific crater lakes confirm new cryptic clades. *The Journal of eukaryotic microbiology*, 71(6), e13060.

Rouzé H, et al. (2024) An integrative phylogeography for inferring cryptic speciation in the *Alpheus lottini* species complex, an important coral mutualist. *iScience*, 27(10), 111034.